

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/596,101A

DATE: 07/18/2001

TIME: 09:29:30

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\07182001\I596101A.raw

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SEP 27 2001

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3 <110> APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL.

5 <120> TITLE OF INVENTION: Peptides and nucleic acids derived from Eisenia foetida and
the use

6 thereof

8 <130> FILE REFERENCE: 2676-4432US

10 <140> CURRENT APPLICATION NUMBER: US 09/596101A

11 <141> CURRENT FILING DATE: 2000-06-16

13 <150> PRIOR APPLICATION NUMBER: PCT/EP98/08169

14 <151> PRIOR FILING DATE: 1998-12-16

16 <150> PRIOR APPLICATION NUMBER: 97203974.7

17 <151> PRIOR FILING DATE: 1997-12-17

19 <160> NUMBER OF SEQ ID NOS: 3

21 <170> SOFTWARE: PatentIn version 3.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 13

25 <212> TYPE: PRT

26 <213> ORGANISM: Eisenia fetida

28 <400> SEQUENCE: 1

30 Ser Gly Glu Ile Asp Ile Ile Glu Thr Ile Gly Asn Arg

31 1 5 10

33 <210> SEQ ID NO: 2

34 <211> LENGTH: 1155

35 <212> TYPE: DNA

36 <213> ORGANISM: Eisenia fetida

38 <220> FEATURE:

39 <221> NAME/KEY: CDS

40 <222> LOCATION: (1)..(1152)

42 <220> FEATURE:

43 <221> NAME/KEY: sig_peptide

44 <222> LOCATION: (1)..(51)

46 <220> FEATURE:

47 <221> NAME/KEY: mat_peptide

48 <222> LOCATION: (52)..()

50 <400> SEQUENCE: 2

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52 Met Arg Trp Thr Leu Val Val Leu Cys Leu Leu Phe Gly Glu Gly Phe

53 -15 -10 -5

55 gcc ttc acc gac tgg gat caa tat cac atc gtc tgg cag gac gaa ttc 96

56 Ala Phe Thr Asp Trp Asp Gln Tyr His Ile Val Trp Gln Asp Glu Phe

57 -1 1 5 10 15

59 gat tac ttt gat ggc gcg aag tgg caa cat gag gtc aca gca act ggc 144

60 Asp Tyr Phe Asp Gly Ala Lys Trp Gln His Glu Val Thr Ala Thr Gly

61 20 25 30

63 gga ggg aac agc gaa ttc caa ctg tac aca cag gat ggg gcc aac agc 192

64 Gly Gly Asn Ser Glu Phe Gln Leu Tyr Thr Gln Asp Gly Ala Asn Ser

65 35 40 45

67 ttc gtt cga gat gga aag ctt ttc att aag ccg acg ttg ctg gct gac 240

68 Phe Val Arg Asp Gly Lys Leu Phe Ile Lys Pro Thr Leu Leu Ala Asp

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69	50	55	60	
71 aac atc aac cca cag acg ggt gcg cca ttt gga acc gat ttc atg tac				288
72 Asn Ile Asn Pro Gln Thr Gly Ala Pro Phe Gly Thr Asp Phe Met Tyr				
73 65 70 75				
75 aat gga gtt cta gat gtc tgg gct atg tac ggg gcc tgc acg aat acg				336
76 Asn Gly Val Leu Asp Val Trp Ala Met Tyr Gly Ala Cys Thr Asn Thr				
77 80 85 90 95				
79 gac aac aac gga tgc tac agg acg gga gcc gct ggc gac att cca ccg				384
80 Asp Asn Asn Gly Cys Tyr Arg Thr Gly Ala Ala Gly Asp Ile Pro Pro				
81 100 105 110				
83 gcc atg tcg gca cga gtt cga acc ttc cag aaa tac agc ttc acc cac				432
84 Ala Met Ser Ala Arg Val Arg Thr Phe Gln Lys Tyr Ser Phe Thr His				
85 115 120 125				
87 gga cgc gtt gtc gtt cac gcc aag atg ccc gtc gga gac tgg ctc tgg				480
88 Gly Arg Val Val Val His Ala Lys Met Pro Val Gly Asp Trp Leu Trp				
89 130 135 140				
91 cca gcc att tgg atg ttg ccg gag gat tgg gtc tat ggc gga tgg cct				528
92 Pro Ala Ile Trp Met Leu Pro Glu Asp Trp Val Tyr Gly Gly Trp Pro				
93 145 150 155				
95 cga tcg ggc gag atc gac atc att gaa aca atc ggc aac cga gat ttc				576
96 Arg Ser Gly Glu Ile Asp Ile Ile Glu Thr Ile Gly Asn Arg Asp Phe				
97 160 165 170 175				
99 aag aac act ggt gga gag ttc ctt gga att cag aag atg gga tca acg				624
100 Lys Asn Thr Gly Gly Glu Phe Leu Gly Ile Gln Lys Met Gly Ser Thr				
101 180 185 190				
103 atg cac tgg ggt cca gga tgg gac gac aac cga tac tgg ctg acc agc				672
104 Met His Trp Gly Pro Gly Trp Asp Asp Asn Arg Tyr Trp Leu Thr Ser				
105 195 200 205				
107 ctt ccg aaa cac tca gac gat tgg aac tac ggt gac aac ttc cac acg				720
108 Leu Pro Lys His Ser Asp Asp Trp Asn Tyr Gly Asp Asn Phe His Thr				
109 210 215 220				
111 ttc tgg ttc gac tgg agt ccc aac gga ctg agg ttc ttc gta gac gac				768
112 Phe Trp Phe Asp Trp Ser Pro Asn Gly Leu Arg Phe Phe Val Asp Asp				
113 225 230 235				
115 gag aac cag gct ctg ctc gat gtt cct tat cct ctg att gat gcg aat				816
116 Glu Asn Gln Ala Leu Leu Asp Val Pro Tyr Pro Leu Ile Asp Ala Asn				
117 240 245 250 255				
119 cca tgg tgg gtg gat ttc tgg gag tgg gga aag ccc tgg ctt cct caa				864
120 Pro Trp Trp Val Asp Phe Trp Glu Trp Gly Lys Pro Trp Leu Pro Gln				
121 260 265 270				
123 tac gaa aat gac aat cca tgg gct gga gga acg aac ctg gct ccc ttc				912
124 Tyr Glu Asn Asp Asn Pro Trp Ala Gly Gly Thr Asn Leu Ala Pro Phe				
125 275 280 285				
127 gac caa aat ttc cac ttc att ctg aac gtg gct gtc gga gga acg aac				960
128 Asp Gln Asn Phe His Phe Ile Leu Asn Val Ala Val Gly Gly Thr Asn				
129 290 295 300				
131 ggc ttc atc ccg gac ggt tgc atc aat cgc ggc gga gac ccg gcc ctg				1008
132 Gly Phe Ile Pro Asp Gly Cys Ile Asn Arg Gly Gly Asp Pro Ala Leu				
133 305 310 315				

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135 cag aag ccg tgg agc aat ggg gac tgg tac aac gat gca atg agg aaa      1056
136 Gln Lys Pro Trp Ser Asn Gly Asp Trp Tyr Asn Asp Ala Met Arg Lys
137 320                               325                               330                               335
139 ttc ttc gac gcc aga gga aac tgg aag tgg acg tgg gat gac gag gga      1104
140 Phe Phe Asp Ala Arg Gly Asn Trp Lys Trp Thr Trp Asp Asp Glu Gly
141                               340                               345                               350
143 gac aac aat gcc atg cag gtc gat tac atc cga gtc tac aag cgc aac      1152
144 Asp Asn Asn Ala Met Gln Val Asp Tyr Ile Arg Val Tyr Lys Arg Asn
145                               355                               360                               365
147 tga                                                                    1155
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 384
152 <212> TYPE: PRT
153 <213> ORGANISM: Eisenia fetida
155 <400> SEQUENCE: 3
157 Met Arg Trp Thr Leu Val Val Leu Cys Leu Leu Phe Gly Glu Gly Phe
158          -15                               -10                               -5
161 Ala Phe Thr Asp Trp Asp Gln Tyr His Ile Val Trp Gln Asp Glu Phe
162 -1 1                               5                               10                               15
165 Asp Tyr Phe Asp Gly Ala Lys Trp Gln His Glu Val Thr Ala Thr Gly
166          20                               25                               30
169 Gly Gly Asn Ser Glu Phe Gln Leu Tyr Thr Gln Asp Gly Ala Asn Ser
170          35                               40                               45
173 Phe Val Arg Asp Gly Lys Leu Phe Ile Lys Pro Thr Leu Leu Ala Asp
174          50                               55                               60
177 Asn Ile Asn Pro Gln Thr Gly Ala Pro Phe Gly Thr Asp Phe Met Tyr
178          65                               70                               75
181 Asn Gly Val Leu Asp Val Trp Ala Met Tyr Gly Ala Cys Thr Asn Thr
182 80                               85                               90                               95
185 Asp Asn Asn Gly Cys Tyr Arg Thr Gly Ala Ala Gly Asp Ile Pro Pro
186          100                               105                               110
189 Ala Met Ser Ala Arg Val Arg Thr Phe Gln Lys Tyr Ser Phe Thr His
190          115                               120                               125
193 Gly Arg Val Val Val His Ala Lys Met Pro Val Gly Asp Trp Leu Trp
194          130                               135                               140
197 Pro Ala Ile Trp Met Leu Pro Glu Asp Trp Val Tyr Gly Gly Trp Pro
198          145                               150                               155
201 Arg Ser Gly Glu Ile Asp Ile Ile Glu Thr Ile Gly Asn Arg Asp Phe
202 160                               165                               170                               175
205 Lys Asn Thr Gly Gly Glu Phe Leu Gly Ile Gln Lys Met Gly Ser Thr
206          180                               185                               190
209 Met His Trp Gly Pro Gly Trp Asp Asp Asn Arg Tyr Trp Leu Thr Ser
210          195                               200                               205
213 Leu Pro Lys His Ser Asp Asp Trp Asn Tyr Gly Asp Asn Phe His Thr
214          210                               215                               220
217 Phe Trp Phe Asp Trp Ser Pro Asn Gly Leu Arg Phe Phe Val Asp Asp
218          225                               230                               235
221 Glu Asn Gln Ala Leu Leu Asp Val Pro Tyr Pro Leu Ile Asp Ala Asn
222 240                               245                               250                               255

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225 Pro Trp Trp Val Asp Phe Trp Glu Trp Gly Lys Pro Trp Leu Pro Gln
226                260                265                270
229 Tyr Glu Asn Asp Asn Pro Trp Ala Gly Gly Thr Asn Leu Ala Pro Phe
230                275                280                285
233 Asp Gln Asn Phe His Phe Ile Leu Asn Val Ala Val Gly Gly Thr Asn
234                290                295                300
237 Gly Phe Ile Pro Asp Gly Cys Ile Asn Arg Gly Gly Asp Pro Ala Leu
238                305                310                315
241 Gln Lys Pro Trp Ser Asn Gly Asp Trp Tyr Asn Asp Ala Met Arg Lys
242 320                325                330                335
245 Phe Phe Asp Ala Arg Gly Asn Trp Lys Trp Thr Trp Asp Asp Glu Gly
246                340                345                350
249 Asp Asn Asn Ala Met Gln Val Asp Tyr Ile Arg Val Tyr Lys Arg Asn
250                355                360                365

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VERIFICATION SUMMARY

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